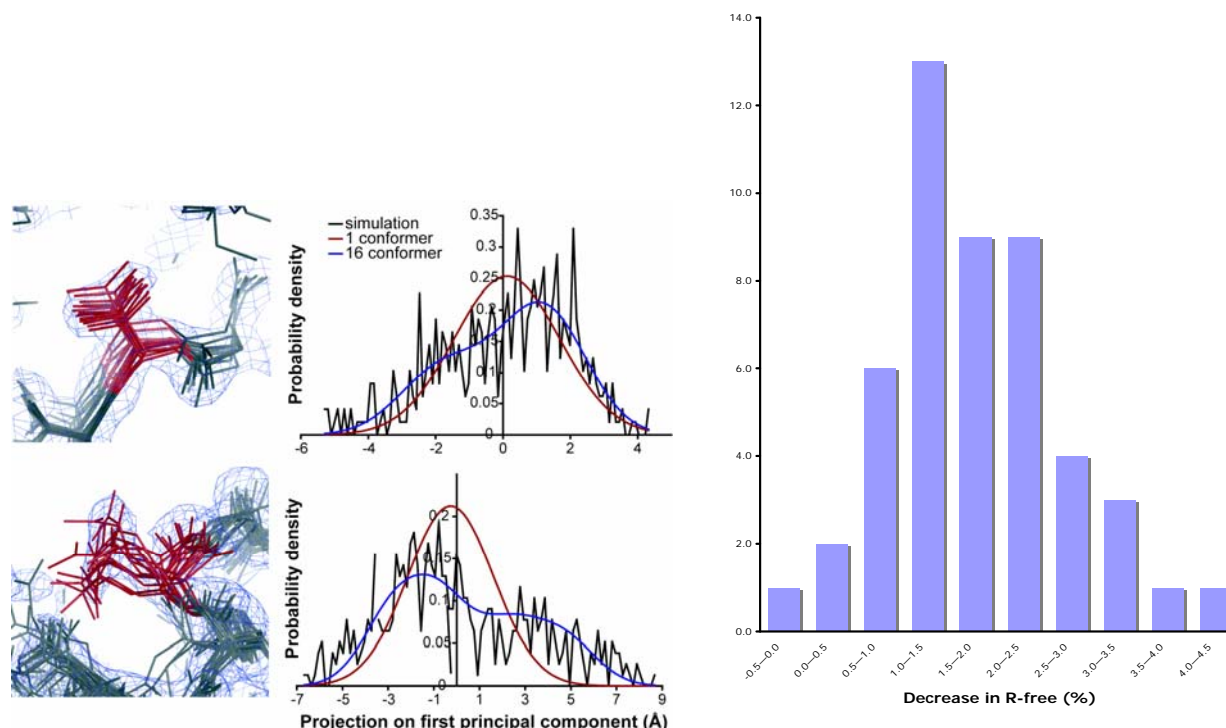


# Center for Eukaryotic Structural Genomics

## Technology Dissemination Report

<b>CESG Tech Report No.</b>	009
<b>Title</b>	<b>Ensemble Refinements of Protein Structures</b>
<b>Research Unit</b>	Crystallography
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### Summary

X-ray crystallography typically uses a single set of coordinates and B-factors to describe macromolecular conformations. Refinement of multiple copies of the entire structure has been previously used in specific cases as an alternative means of representing structural flexibility. We have developed a fully automated implementation of this approach and have systematically validated it using simulated diffraction data, and find that ensemble refinement produces better representations of the distributions of atomic positions in the simulated structures than single conformer refinements, and can accurately model anharmonic and multi-modal motions (left figure).[1] Comparison of principal components calculated from the refined ensembles and simulations shows that concerted motions are captured locally, but correlations dissipate over long distances. The technique was also tested on 50 experimental structures of varying resolution, and led to decreases in R-free (right figure), implying that improvements in the representation of flexibility observed for the simulated structures may apply to real structures. These gains were essentially independent of resolution or data-to-parameter ratio, suggesting even structures at moderate resolution can benefit from ensemble refinement.

Publication:

[1] Levin, E.J., Kondrashov, D.A., Wesenberg, G.E., and Phillips, G.N., Jr. (2007) Ensemble refinement of protein crystal structures: validation and application. *Structure* 15:1040-1052.

### Acquiring the Technology

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### Other Acknowledgements

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